WE CLAIM:

1. A database comprising the nucleotide sequences of a plurality of cDNA molecules selected for the analysis of hematopoietic tissue, said tissue including bone marrow, peripheral blood, stem cells, transplanted marrow, and leukemia cells from human and related primates including baboon.

2. The database of claim 1 comprising molecules having the nucleotide sequences designated by the unique identifiers as shown in Appendix A.

3. A microchip comprising the database of claim 1 or a subset thereof.

4. A method for selecting a database containing expressed genes from primate CD34+ cells, said method comprising:

    (a) selecting genes whose expression level is greater than or equal to 7-fold above background in human cells; and

    (b) further selecting genes selected in (a) whose expression levels differ between humans and baboons by 3-fold or less.

5. The method of claim 4, wherein gene expression is measured by the gene filter method.

6. A computer system comprising:

    (a) a database containing nucleotide sequences pertaining to a plurality of biomolecular sequences selected in accord with the method of claim 4;

    (b) a first hierarchy of function categories into which at least some of said biomolecular sequences are grouped;

    (c) a user interface allowing a user to selectively view information regarding said plurality of said biomolecular sequences as it relates to said first hierarchy.

7. The computer system of claim 7, wherein the biomolecular sequences are selected from the group consisting of ESTs, full-length sequences, and combinations thereof.

8. The computer system of claim 7, wherein the user interface allows the user to selectively view information regarding a subset of said plurality of said biomolecular sequences which subset is grouped in both a selected category and for a selected application.

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9.   A computer-implemented method for managing information relating to hematopoietic analyses said method comprising:

    (a)   a first identifier identifying a target sample applied to a probe array chip;

    (b)   a second identifier identifying said probe array chip to which said target sample was applied; and

    (b)   creating an electronically-stored chip table, said chip table storing a record for said polymer probe array chip, said chip record comprising

        (i)   a plurality of fields storing at least one of a plurality of data identifiers, including:

        (ii)   said second identifier identifying said probe array chip, and

        (iii)   a third identifier specifying a layout of probes on said probe array chip.

10.   A database method for analyzing hematopoetic tissue said method comprising:

    (a)   providing a first database comprising a first plurality of records, one for each of a plurality of cDNA sequences, said records having at least one of a plurality of fields storing:

        (i)   a first attribute identifying a target sample applied to a probe array chip;

        (ii)   a second attribute identifying said probe array chip to which said target sample was applied; and

    (b)   providing a second database comprising a second plurality of records for said probe array chip, said records having at least one of a plurality of fields storing:

        (i)   said second attribute identifying said probe array chip; and

        (ii)   a third attribute specifying a layout of probes on said probe array chip.

11.   The database method for analyzing gene expression information of claim 10, wherein said first database and said second database are relational database tables.